

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/517,939
Source: PCT
Date Processed by STIC: 08/22/2005

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 08/22/2005

PATENT APPLICATION: US/10/517,939

TIME: 17:01:01

Input Set : D:\56446-20079.01 - Seqlist (client).txt

Output Set: N:\CRF4\08222005\J517939.raw

4 <110> APPLICANT: Steer, Brian
 5 Callen, Walter
 6 Healey, Shaun
 7 Hazlewood, Geoff
 8 Wu, Di
 9 Blum, David
 10 Esteghlalian, Alireza
 12 <120> TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
 13 AND METHODS FOR MAKING AND USING THEM
 15 <130> FILE REFERENCE: 564462007901
 17 <140> CURRENT APPLICATION NUMBER: 10/517,939
 C--> 18 <141> CURRENT FILING DATE: 2004-12-13
 20 <150> PRIOR APPLICATION NUMBER: PCT/US03/19153
 21 <151> PRIOR FILING DATE: 2003-06-16
 23 <150> PRIOR APPLICATION NUMBER: 60/389,299
 24 <151> PRIOR FILING DATE: 2002-06-14
 26 <160> NUMBER OF SEQ ID NOS: 380
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 1128
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Bacteria
 35 <400> SEQUENCE: 1
 36 atgaccgacc acaacgcttc cgaaaccagc ctgttcgaac agtgccggcta cagccgcgag 60
 37 gccatccagg ccgcgcctga gcgcaactgg tatgagatgt tcgaaggccc ggacaagatt 120
 38 tactggggaga acgacgaagg cctgggggtac gtgatggaca ccggcaacca cgacgtgcgc 180
 39 accgaggggca tgagctacgc gatgatgata gccgtgcagt acggccgcaa ggacgtgttc 240
 40 gacaagctgt ggggttgggt catgaaatac atgttcatga ccgagggcct gcaccagggc 300
 41 tacttcgcct ggtctgtgga ccccgagcgc gtaccgaacg ccgacgggtc ggccccggac 360
 42 ggcgaggaat acttcgcgat ggacctgttc ctggcctccg cgcgatgggg cgacggcgaa 420
 43 ggcgtgtacg agtactcccg ccacgcccgc tgcatactcc acacctgcgt gcaccagggc 480
 44 gaggacgggtg aaggctatcc gatgtggaac ccggagaacc atctgatcaa gttcatcccg 540
 45 gaaaccgaat ggaccgaccc gtcctaccat ctgccgcact tctacgaggt gttcgccgag 600
 46 cgcgcgcgacg aggcgcgacg tccgttctgg gcgcaggccg ccaaggcgag ccgcgagtac 660
 47 ctgggtcaccg cctgccaccc gcgaccggc atgaaccccg aataactcaa ctatgatggc 720
 48 acgcgcgacg tcgacgagcg cgaccactgg catttctact ccgacgccta ccgcaccgcc 780
 49 ggcaacatcg ggctggactg cctgtggaac ggcgtcgtgc cggaactgtg cgatgcgaat 840
 50 gcgcgtctgc agcgtttctt cctcgaaac gaccgcacct gcgtgtatgc gatcgacggc 900
 51 acgcgggtgg acgagaccgt gctgcacccg gtcgggttca tcgccgccac cgccgaaggc 960
 52 tcgctcgccg cgatgcactc gcaggagccg gacgcgctcg acaacgcgat ccgctgggtg 1020
 53 cgctgctgtg gggacacccc gatccgcacc ggcacgcgcc gctactacga caacttcctc 1080
 54 tacgccttcg cgttcctggc gctggcgggg gactaccgca cctgggtga 1128
 56 <210> SEQ ID NO: 2

RAW SEQUENCE LISTING

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57 <211> LENGTH: 375
58 <212> TYPE: PRT
59 <213> ORGANISM: Bacteria
61 <400> SEQUENCE: 2
62 Met Thr Asp His Asn Ala Ser Glu Thr Ser Leu Phe Glu Gln Cys Gly
63 1 5 10 15
64 Tyr Ser Arg Glu Ala Ile Gln Ala Arg Leu Glu Arg Asn Trp Tyr Glu
65 20 25 30
66 Met Phe Glu Gly Pro Asp Lys Ile Tyr Trp Glu Asn Asp Glu Gly Leu
67 35 40 45
68 Gly Tyr Val Met Asp Thr Gly Asn His Asp Val Arg Thr Glu Gly Met
69 50 55 60
70 Ser Tyr Ala Met Met Ile Ala Val Gln Tyr Gly Arg Lys Asp Val Phe
71 65 70 75 80
72 Asp Lys Leu Trp Gly Trp Val Met Lys Tyr Met Phe Met Thr Glu Gly
73 85 90 95
74 Leu His Gln Gly Tyr Phe Ala Trp Ser Val Asp Pro Ser Gly Val Pro
75 100 105 110
76 Asn Ala Asp Gly Pro Ala Pro Asp Gly Glu Glu Tyr Phe Ala Met Asp
77 115 120 125
78 Leu Phe Leu Ala Ser Ala Arg Trp Gly Asp Gly Glu Gly Val Tyr Glu
79 130 135 140
80 Tyr Ser Arg His Ala Arg Ser Ile Leu His Thr Cys Val His Gln Gly
81 145 150 155 160
82 Glu Asp Gly Glu Gly Tyr Pro Met Trp Asn Pro Glu Asn His Leu Ile
83 165 170 175
84 Lys Phe Ile Pro Glu Thr Glu Trp Thr Asp Pro Ser Tyr His Leu Pro
85 180 185 190
86 His Phe Tyr Glu Val Phe Ala Glu Arg Ala Asp Glu Ala Asp Arg Pro
87 195 200 205
88 Phe Trp Ala Gln Ala Ala Lys Ala Ser Arg Glu Tyr Leu Val Thr Ala
89 210 215 220
90 Cys His Pro Gln Thr Gly Met Asn Pro Glu Tyr Ser Asn Tyr Asp Gly
91 225 230 235 240
92 Thr Pro His Val Asp Glu Arg Asp His Trp His Phe Tyr Ser Asp Ala
93 245 250 255
94 Tyr Arg Thr Ala Gly Asn Ile Gly Leu Asp Cys Leu Trp Asn Gly Val
95 260 265 270
96 Val Pro Glu Leu Cys Asp Ala Asn Ala Arg Leu Gln Arg Phe Phe Leu
97 275 280 285
98 Glu His Asp Arg Thr Cys Val Tyr Ala Ile Asp Gly Thr Pro Val Asp
99 290 295 300
100 Glu Thr Val Leu His Pro Val Gly Phe Ile Ala Ala Thr Ala Glu Gly
101 305 310 315 320
102 Ser Leu Ala Ala Met His Ser Gln Glu Pro Asp Ala Leu Asp Asn Ala
103 325 330 335
104 Ile Arg Trp Val Arg Leu Leu Trp Asp Thr Pro Ile Arg Thr Gly Thr
105 340 345 350
106 Arg Arg Tyr Tyr Asp Asn Phe Leu Tyr Ala Phe Ala Phe Leu Ala Leu

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107          355          360          365
108 Ala Gly Glu Tyr Arg Thr Trp
109          370          375
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112 <211> LENGTH: 2196
113 <212> TYPE: DNA
114 <213> ORGANISM: Unknown
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Obtained from an environmental sample
119 <400> SEQUENCE: 3
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121 aacaaactgt ttgttaacgg ggtggaatcc ggagataatg ccgaaagaat ctatgtagag      120
122 actggaagcg acatggcgta catccatacc tttgacagca acgacgtgcg ctccgaagga      180
123 atgtcctacg gcatgatgat gtgcgtagac atgaacgac agacaagatt taacaaactc      240
124 tggaaatggg caagaaccta tatgtacaat gaaacagacg ccggcagtaa ttccaggggc      300
125 tatttctcat ggcagtgcag tacaagcggc tcaaaaatgg ataagggccc cgctcctgac      360
126 ggcgaggaat actttattac ggcgctgttg ttgcgcgacg ccgctggggg ggcgcgctcc      420
127 ggtactacaa acataaacia ttacgcgcag caagcaaggc agattatcta tgacttaacg      480
128 cgccgcaaac cggggaacgg agatccttac ggcgagcctt caatgtttaa tgtagacaac      540
129 tatatgggta gattcgccac acttggaat tccgccacct ttacagaccc ctcataccat      600
130 ttaccggcat tctatgatgt ttgggcgtg gaattacagg cggactatga taatagtaaa      660
131 ctctacggta tctgggctga taaggctgac ttgaaaaaag acattgatta ctttaacaa      720
132 gcggcgacca caagccgttc attctttgca aaaacgacaa acggtacaac cggacttgga      780
133 ccggattatg ccggctttga cggaacgcct aaaaatgaag gggatcacia gtatttcgag      840
134 tatgacgcgt ggcgtatcgc gatgaacata ggtatggact acgcgtgggt cgcgaaagat      900
135 tcctggcgag agacatttgc cgacagaatt caggcgcttct ttgtcagcaa gggagtcaat      960
136 tcttacggaa accgctggac attggacggg actcaaaggg gagcggatca ctgcgccggg      1020
137 cttgtcggtt gtaacgcggg cgctctctc gcggcgacaa acgcgaacgc gtggaaattt      1080
138 atcgaagact tctggaacat cagcatgacg aaaggcaaat accgttacta tgacggatgt      1140
139 ctgtatatga tgagcatgct gcaacttaagc ggcaacttta aggcgtatct ttctacaaat      1200
140 accacgcccg ccaacagttc cagcattacc ccgacaaccg cgtctttcga caagaagaca      1260
141 agcgcacaag ccgacattgc cgtaacagtg acgcttaacg ggaatacatt ctcaagtatc      1320
142 acaaaacacg gtacgcctt tacaagcggc acagactact cagtgagtgg aacaaagtat      1380
143 acgataaaga agaatacct tgcaaaacag cctgtaggaa caacgaagct cgcattcaac      1440
144 ttcagtgcgg gaggaactcc ggaacttaca gttactataa cggacacggg cagctccagc      1500
145 atcagcccga caaccgcgac attcgacaaa aagaccggag cgcaagccga catcgccgta      1560
146 accatgacgc ttaatgggaa tactttgtcg aacatcaaaa acggttctgc acaacttaca      1620
147 agcgggaactg actactcaac gagcggcagt acggtaacga ttaaaaaaga atacctggca      1680
148 aagcaggcta acggcacagt aacgcttacc ttcacattca gcgcaggcgc ggcccaaact      1740
149 attgacatca cggtaaaaga tacaaccggc ggagcggcgg gaataaaata caacttcgca      1800
150 actgacaacc tgcccaacgg gtaccggaag tacagttcaa gtgatatac cgcgacaata      1860
151 accggaggag ctttggtaat aacccaaacc ggaaataatt cgtccccgaa gattacattg      1920
152 cccttttagt taacaggtaa cctttccggg tatacaggca taaagataaa tgtaaaggga      1980
153 gtatccggag atttcaacta taaagtattg aatgccgcaa taggttctac aaatctcggc      2040
154 agcgtaaata acgccccaat accaaacggc tcatttggag acgtaacaat accaataacc      2100
155 ggcggtacaa acaccggaga tttagatata tcgttctggc tcaataacac aaatgcttac      2160
156 gttattgaga ttaagagcat agagctggtg aatatga      2196
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 711

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160 <212> TYPE: PRT
161 <213> ORGANISM: Unknown
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Obtained from an environmental sample
166 <400> SEQUENCE: 4
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168 1 5 10 15
169 Asn Thr Ala Trp Asn Lys Leu Phe Val Asn Gly Val Glu Ser Gly Asp
170 20 25 30
171 Asn Ala Glu Arg Ile Tyr Val Glu Thr Gly Ser Asp Met Ala Tyr Ile
172 35 40 45
173 His Thr Phe Asp Ser Asn Asp Val Arg Ser Glu Gly Met Ser Tyr Gly
174 50 55 60
175 Met Met Met Cys Val Gln Met Asn Asp Gln Thr Arg Phe Asn Lys Leu
176 65 70 75 80
177 Trp Lys Trp Ala Arg Thr Tyr Met Tyr Asn Glu Thr Asp Ala Gly Ser
178 85 90 95
179 Asn Ser Arg Gly Tyr Phe Ser Trp Gln Cys Ser Thr Ser Gly Ser Lys
180 100 105 110
181 Met Asp Lys Gly Pro Ala Pro Asp Gly Glu Glu Tyr Phe Ile Thr Ala
182 115 120 125
183 Leu Leu Phe Ala His Ala Arg Trp Gly Ser Ala Ser Gly Thr Thr Asn
184 130 135 140
185 Ile Asn Asn Tyr Ala Gln Gln Ala Arg Gln Ile Ile Tyr Asp Leu Thr
186 145 150 155 160
187 Arg Arg Lys Pro Gly Asn Gly Asp Pro Tyr Gly Glu Pro Ser Met Phe
188 165 170 175
189 Asn Val Asp Asn Tyr Met Val Arg Phe Ala Thr Leu Gly Asn Ser Ala
190 180 185 190
191 Thr Phe Thr Asp Pro Ser Tyr His Leu Pro Ala Phe Tyr Asp Val Trp
192 195 200 205
193 Ala Leu Glu Leu Gln Ala Asp Tyr Asp Asn Ser Lys Leu Tyr Gly Ile
194 210 215 220
195 Trp Ala Asp Lys Ala Asp Leu Lys Lys Asp Ile Asp Tyr Phe Lys Gln
196 225 230 235 240
197 Ala Ala Thr Thr Ser Arg Ser Phe Phe Ala Lys Thr Thr Asn Gly Thr
198 245 250 255
199 Thr Gly Leu Gly Pro Asp Tyr Ala Gly Phe Asp Gly Thr Pro Lys Asn
200 260 265 270
201 Glu Gly Asp His Lys Tyr Phe Glu Tyr Asp Ala Trp Arg Ile Ala Met
202 275 280 285
203 Asn Ile Gly Met Asp Tyr Ala Trp Phe Ala Lys Asp Ser Trp Gln Lys
204 290 295 300
205 Thr Phe Ala Asp Arg Ile Gln Ala Phe Phe Val Ser Lys Gly Val Thr
206 305 310 315 320
207 Ser Tyr Gly Asn Arg Trp Thr Leu Asp Gly Thr Gln Arg Gly Ala Asp
208 325 330 335
209 His Ser Pro Gly Leu Val Gly Cys Asn Ala Val Ala Ser Leu Ala Ala
210 340 345 350 ,

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211 Thr Asn Ala Asn Ala Trp Lys Phe Ile Glu Asp Phe Trp Asn Ile Ser
212      355      360      365
213 Met Thr Lys Gly Lys Tyr Arg Tyr Tyr Asp Gly Cys Leu Tyr Met Met
214      370      375      380
215 Ser Met Leu His Leu Ser Gly Asn Phe Lys Ala Tyr Leu Ser Thr Asn
216 385      390      395      400
217 Thr Thr Pro Ala Asn Ser Ser Ser Ile Thr Pro Thr Thr Ala Ser Phe
218      405      410      415
219 Asp Lys Lys Thr Ser Ala Gln Ala Asp Ile Ala Val Thr Val Thr Leu
220      420      425      430
221 Asn Gly Asn Thr Phe Ser Ser Ile Thr Asn Asn Gly Thr Ala Leu Thr
222      435      440      445
223 Ser Gly Thr Asp Tyr Ser Val Ser Gly Thr Lys Tyr Thr Ile Lys Lys
224      450      455      460
225 Glu Tyr Leu Ala Lys Gln Pro Val Gly Thr Thr Lys Leu Ala Phe Asn
226 465      470      475      480
227 Phe Ser Ala Gly Gly Thr Pro Glu Leu Thr Val Thr Ile Thr Asp Thr
228      485      490      495
229 Gly Ser Ser Ser Ile Ser Pro Thr Thr Ala Thr Phe Asp Lys Lys Thr
230      500      505      510
231 Gly Ala Gln Ala Asp Ile Ala Val Thr Met Thr Leu Asn Gly Asn Thr
232      515      520      525
233 Leu Ser Asn Ile Lys Asn Gly Ser Ala Gln Leu Thr Ser Gly Thr Asp
234      530      535      540
235 Tyr Ser Thr Ser Gly Ser Thr Val Thr Ile Lys Lys Glu Tyr Leu Ala
236 545      550      555      560
237 Lys Gln Ala Asn Gly Thr Val Thr Leu Thr Phe Thr Phe Ser Ala Gly
238      565      570      575
239 Ala Ala Gln Thr Ile Asp Ile Thr Val Lys Asp Thr Thr Gly Gly Ala
240      580      585      590
241 Ala Gly Ile Lys Tyr Asn Phe Ala Thr Asp Asn Leu Pro Asn Gly Tyr
242      595      600      605
243 Pro Lys Tyr Ser Ser Ser Asp Ile Ser Ala Thr Ile Thr Gly Gly Ala
244      610      615      620
245 Leu Val Ile Thr Lys Thr Gly Asn Asn Ser Ser Pro Lys Ile Thr Leu
246 625      630      635      640
247 Pro Phe Ser Val Thr Gly Asn Leu Ser Gly Tyr Thr Gly Ile Lys Ile
248      645      650      655
249 Asn Val Lys Gly Val Ser Gly Asp Phe Thr Tyr Lys Val Leu Asn Ala
250      660      665      670
251 Ala Ile Gly Ser Thr Asn Leu Gly Ser Val Asn Asn Ala Pro Ile Pro
252      675      680      685
253 Asn Gly Ser Phe Gly Asp Val Thr Ile Pro Ile Thr Gly Gly Thr Asn
254      690      695      700
255 Thr Gly Asp Leu Asp Ile Ser
256 705      710
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 2106
260 <212> TYPE: DNA

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VERIFICATION SUMMARY

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Input Set : D:\56446-20079.01 - Seqlist (client).txt

Output Set: N:\CRF4\08222005\J517939.raw

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:312 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:315 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:449 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:452 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:558 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:561 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:658 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:661 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:834 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:837 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1005 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1008 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
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L:1098 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:1185 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
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L:1358 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:1697 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1700 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:2154 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:40
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L:2461 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:46
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L:2754 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:52
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L:3087 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:56
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L:3185 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
L:3290 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:3670 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:68
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L:3772 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:70
L:4031 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4034 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:74
L:4259 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

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L:4262 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:76
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L:4451 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:80
L:4657 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:84
L:4914 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4917 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:88
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L:5334 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:96
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L:5527 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:100
L:5612 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5615 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:102
L:5708 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5709 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:5840 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5843 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:106
L:6117 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:6120 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:110
L:6297 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:6300 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:114
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L:6619 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:120
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L:6782 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:122
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L:6905 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:124
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L:7525 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:136
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L:7790 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:142
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L:8202 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:148
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L:8291 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:150
L:8374 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:152
L:8462 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8465 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:154
L:8560 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8563 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:156
L:8672 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8675 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:158

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L:8741 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8744 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:160
L:8829 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:162
L:8914 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:164